

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/782,953

DATE: 03/12/2001  
TIME: 12:41:32

Input Set : A:\UTSD674US.txt  
Output Set: N:\CRF3\03122001\I782953.raw

ENTERED

3 <110> APPLICANT: WILLIAMS, R. SANDERS  
4 ROTHERMEL, BEVERLY  
6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SELECTIVE  
7 CALCINEURIN INTERACTING PROTEIN (MCIP)  
9 <130> FILE REFERENCE: UTSD:674PZ1  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/782,953  
12 <141> CURRENT FILING DATE: 2001-02-13  
14 <150> PRIOR APPLICATION NUMBER: 60/216,601  
15 <151> PRIOR FILING DATE: 2000-07-07  
17 <160> NUMBER OF SEQ ID NOS: 27  
19 <170> SOFTWARE: PatentIn Ver. 2.1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 599  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Mus musculus  
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28 ctgccccgtg aaaaagcaga atgatttttag ggacttttagc tacaatttta gctccctgat 120  
29 tgcttggtgtg gcaaacgatg atgtcttcag cgaaagttag accagggcca aatttgaatc 180  
30 cctcttcaga acatatgaca aggacaccac cttocagtat tttaagagct tcaaacgtgt 240  
31 cgggataaac ttcagcaaac ccttatctgc agccgatgcc aggctgcggc tgcacaagac 300  
32 cgagttcctg ggggaaggaaa tgaagttgta ttttgctcag actttacaca taggaagttc 360  
33 acacctggct ccgccaatcc cgacaaacag ttcctcatct cccctccggc ctctcctccc 420  
34 gttggctgga aacaagtaga agatgccacc cccgtcataa attacgatct tttatatgcc 480  
35 atctccaagc tggggccagg agagaagtat gaactgcatg cagcgacaga caccactccc 540  
36 agtgtggtgg tccacgtgtg tgagagtgac caagagaatg aggaggaaga ggaagagat 599  
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42 <213> ORGANISM: Mus musculus  
44 <220> FEATURE:  
45 <221> NAME/KEY: CDS  
46 <222> LOCATION: (1)..(594)  
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50 Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys  
51 1 5 10 15  
53 cac ctg gac ccg cgc gtg ttc gtg gac ggc ctg tgc cgg gcc aaa ttt 96  
54 His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe  
55 20 25 30  
57 gaa tcc ctc ttc aga aca tat gac aag gac acc acc ttc cag tat ttt 144  
58 Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe  
59 35 40 45  
61 aag agc ttc aaa cgt gtc cgg ata aac ttc agc aac ccc tta tct gca 192  
62 Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala  
63 50 55 60  
65 gcc gat gcc agg ctg cgg ctg cac aag acc gag ttc ctg ggg aag gaa 240

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66 Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
67 65 70 75 80
69 atg aag ttg tat ttt gct cag act tta cac ata gga agt tca cac ctg 288
70 Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
71 85 90 95
73 gct ccg ccc aat ccc gac aaa cag ttc ctc atc tcc cct ccg gcc tct 336
74 Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
75 100 105 110
77 cct ccc gtt ggc tgg aaa caa gta gaa gat gcc acc ccc gtc ata aat 384
78 Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
79 115 120 125
81 tac gat ctt tta tat gcc atc tcc aag ctg ggg cca gga gag aag tat 432
82 Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
83 130 135 140
85 gaa ctg cat gca gcg aca gac ccc act ccc agt gtg gtc cac gtg 480
86 Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
87 145 150 155 160
89 tgt gag agt gac caa gag aat gag gag gaa gag gaa gag atg gag aga 528
90 Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
91 165 170 175
93 atg aag aga ccc aag ccc aaa atc atc cag aca cgg aga ccg gag tac 576
94 Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
95 180 185 190
97 aca ccg atc cac ctt agc tga 597
98 Thr Pro Ile His Leu Ser
99 195
102 <210> SEQ ID NO: 3
103 <211> LENGTH: 198
104 <212> TYPE: PRT
105 <213> ORGANISM: Mus musculus
107 <400> SEQUENCE: 3
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109 1 5 10 15
111 His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
112 20 25 30
114 Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
115 35 40 45
117 Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
118 50 55 60
120 Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
121 65 70 75 80
123 Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
124 85 90 95
126 Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
127 100 105 110
129 Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
130 115 120 125
132 Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
133 130 135 140

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135 Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
136 145          150          155          160
138 Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
139          165          170          175
141 Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
142          180          185          190
144 Thr Pro Ile His Leu Ser
145          195
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150 <211> LENGTH: 198
151 <212> TYPE: PRT
152 <213> ORGANISM: Mus musculus
154 <400> SEQUENCE: 4
155 Met Glu Glu Val Asp Leu Gln Asp Leu Pro Ser Ala Thr Ile Ala Cys
156 1          5          10          15
158 His Leu Asp Pro Arg Val Phe Val Asp Gly Leu Cys Arg Ala Lys Phe
159          20          25          30
161 Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
162          35          40          45
164 Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
165          50          55          60
167 Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
168 65          70          75          80
170 Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
171          85          90          95
173 Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
174          100          105          110
176 Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
177          115          120          125
179 Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
180          130          135          140
182 Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
183 145          150          155          160
185 Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
186          165          170          175
188 Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
189          180          185          190
191 Thr Pro Ile His Leu Ser
192          195
195 <210> SEQ ID NO: 5
196 <211> LENGTH: 597
197 <212> TYPE: DNA
198 <213> ORGANISM: Mus musculus
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (1)..(594)
204 <400> SEQUENCE: 5
205 atg gat ttt agg gac ttt agc tac aat ttt agc tcc ctg att gct tgt 48
206 Met Asp Phe Arg Asp Phe Ser Tyr Asn Phe Ser Ser Leu Ile Ala Cys

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207   1           5           10           15
209 gtg gca aac gat gat gtc ttc agc gaa agt gag acc agg gcc aaa ttt   96
210 Val Ala Asn Asp Asp Val Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe
211           20           25           30
213 gaa tcc ctc ttc aga aca tat gac aag gac acc acc ttc cag tat ttt   144
214 Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
215           35           40           45
217 aag agc ttc aaa cgt gtc cgg ata aac ttc agc aac ccc tta tct gca   192
218 Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
219           50           55           60
221 gcc gat gcc agg ctg cgg ctg cac aag acc gag ttc ctg ggg aag gaa   240
222 Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
223   65           70           75           80
225 atg aag ttg tat ttt gct cag act tta cac ata gga agt tca cac ctg   288
226 Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
227           85           90           95
229 gct ccg ccc aat ccc gac aaa cag ttc ctc atc tcc cct ccg gcc tct   336
230 Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
231           100           105           110
233 cct ccc gtt ggc tgg aaa caa gta gaa gat gcc acc ccc gtc ata aat   384
234 Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
235           115           120           125
237 tac gat ctt tta tat gcc atc tcc aag ctg ggg cca gga gag aag tat   432
238 Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
239           130           135           140
241 gaa ctg cat gca gcg aca gac ccc act ccc agt gtg gtg gtc cac gtg   480
242 Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
243 145           150           155           160
245 tgt gag agt gac caa gag aat gag gag gaa gag gaa gag atg gag aga   528
246 Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Glu Met Glu Arg
247           165           170           175
249 atg aag aga ccc aag ccc aaa atc atc cag aca cgg aga ccg gag tac   576
250 Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
251           180           185           190
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254 Thr Pro Ile His Leu Ser
255           195
258 <210> SEQ ID NO: 6
259 <211> LENGTH: 198
260 <212> TYPE: PRT
261 <213> ORGANISM: Mus musculus
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267 Val Ala Asn Asp Asp Val Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe
268           20           25           30
270 Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
271           35           40           45
273 Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala

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274      50      55      60
276 Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
277 65      70      75      80
279 Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
280      85      90      95
282 Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
283      100      105      110
285 Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
286      115      120      125
288 Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
289      130      135      140
291 Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
292 145      150      155      160
294 Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
295      165      170      175
297 Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
298      180      185      190
300 Thr Pro Ile His Leu Ser
301      195
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306 <211> LENGTH: 198
307 <212> TYPE: PRT
308 <213> ORGANISM: Mus musculus
310 <400> SEQUENCE: 7
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314 Val Ala Asn Asp Val Phe Ser Glu Ser Glu Thr Arg Ala Lys Phe
315      20      25      30
317 Glu Ser Leu Phe Arg Thr Tyr Asp Lys Asp Thr Thr Phe Gln Tyr Phe
318      35      40      45
320 Lys Ser Phe Lys Arg Val Arg Ile Asn Phe Ser Asn Pro Leu Ser Ala
321      50      55      60
323 Ala Asp Ala Arg Leu Arg Leu His Lys Thr Glu Phe Leu Gly Lys Glu
324 65      70      75      80
326 Met Lys Leu Tyr Phe Ala Gln Thr Leu His Ile Gly Ser Ser His Leu
327      85      90      95
329 Ala Pro Pro Asn Pro Asp Lys Gln Phe Leu Ile Ser Pro Pro Ala Ser
330      100      105      110
332 Pro Pro Val Gly Trp Lys Gln Val Glu Asp Ala Thr Pro Val Ile Asn
333      115      120      125
335 Tyr Asp Leu Leu Tyr Ala Ile Ser Lys Leu Gly Pro Gly Glu Lys Tyr
336      130      135      140
338 Glu Leu His Ala Ala Thr Asp Pro Thr Pro Ser Val Val Val His Val
339 145      150      155      160
341 Cys Glu Ser Asp Gln Glu Asn Glu Glu Glu Glu Glu Met Glu Arg
342      165      170      175
344 Met Lys Arg Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Glu Tyr
345      180      185      190
347 Thr Pro Ile His Leu Ser

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VERIFICATION SUMMARY

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